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M P S R E L H  
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(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Aug 6 14:06:36 1998; MasPar time 11.35 Seconds  
Tabular output not generated. 781.822 Million cell updates/sec

Title: >US-08-813-323A-1  
Description: (324-566) from US0881323A.pap (3 of 3)  
Sequence: 1 SOAEKLKELDKIRPFQNW.....YIKDDTIFIKIVDTSDLPD 243

Scoring table: PAM 150  
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir56  
1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 45.997; Variance 110.625; scale 0.416

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		Match		Length		DB		ID		Description		Pred. No.	
1	1764	100.0	567	2	I49272	CD40 receptor-associat	3.34e-278								
2	1754	99.4	568	2	A55960	CD40 receptor-associat	1.93e-276								
3	1754	99.4	568	2	A55649	TNFR-associated prote	1.93e-276								
4	1747	99.0	543	2	I53498	CD40-associated prote	3.29e-275								
5	811	46.0	501	2	I51512	TNF receptor associat	3.24e-112								
6	793	45.0	501	2	S56163	tumor necrosis factor	3.84e-109								
7	730	41.4	416	2	B55649	TNFR-associated prote	2.05e-98								
8	728	41.3	409	2	A54750	TNF receptor associat	4.48e-98								
9	437	24.8	470	2	I38026	MLN 62 protein - huma	1.59e-49								
10	164	9.3	760	2	A40195	meprin A (EC 3.4.24.1	7.39e-08								
11	151	8.6	748	2	S24134	endopeptidase 2 (EC 3	3.80e-06								
12	135	7.7	746	1	HKHDA	meprin A (EC 3.4.24.1	7.39e-08								
13	132	7.5	700	1	HYHMB	meprin A (EC 3.4.24.1	4.05e-04								
14	128	7.3	283	2	A60364	tropomyosin - migrato	2.90e-03								
15	121	6.9	668	2	A42908	meprin A (EC 3.4.24.1	1.98e-02								
16	119	6.7	704	2	A48040	meprin beta chain pre	3.39e-02								
17	116	6.6	285	2	A25561	tropomyosin II, muscl	7.52e-02								
18	114	6.5	284	2	A45488	body-wall muscle trop	1.27e-01								
19	114	6.5	284	2	A45488	tropomyosin, fast mus	1.27e-01								
20	113	6.4	245	2	C34787	tropomyosin 3 alpha,	1.65e-01								
21	113	6.4	248	2	C39816	tropomyosin 5a, fibro	1.65e-01								
22	113	6.4	248	2	D39816	tropomyosin 5b, fibro	1.65e-01								
23	113	6.4	251	2	B34787	tropomyosin 2 alpha,	1.65e-01								

24	113	6.4	535	2	S74703	hypothetical protein	1.65e-01								
25	113	6.4	4096	2	A57099	DNA-activated protein	1.65e-01								
26	111	6.3	847	2	A53800	mixed-lineage protein	2.78e-01								
27	111	6.3	1060	2	S63993	acrosomal protein AZ1	2.78e-01								
28	109	6.2	214	2	I40303	outer membrane lipopr	4.63e-01								
29	109	6.2	227	2	S05585	tropomyosin - human	4.63e-01								
30	110	6.2	284	2	S38381	tropomyosin - Califor	3.59e-01								
31	107	6.1	243	2	S55467	tropomyosin isoform -	7.70e-01								
32	107	6.1	280	2	A22165	tropomyosin alpha cha	7.70e-01								
33	107	6.1	281	2	A34787	tropomyosin 1 alpha,	7.70e-01								
34	107	6.1	284	5	2TMAB	tropomyosin alpha cha	7.70e-01								
35	107	6.1	284	1	2MRSA	tropomyosin alpha cha	7.70e-01								
36	107	6.1	284	5	2TMAB	tropomyosin alpha cha	7.70e-01								
37	107	6.1	284	2	A25825	tropomyosin alpha cha	7.70e-01								
38	107	6.1	284	2	B27407	tropomyosin alpha cha	7.70e-01								
39	107	6.1	284	2	S24972	tropomyosin alpha cha	7.70e-01								
40	107	6.1	284	2	A27674	tropomyosin 3, fibrob	7.70e-01								
41	107	6.1	284	2	A39816	tropomyosin 2, fibrob	7.70e-01								
42	107	6.1	284	2	A60597	tropomyosin 3, fibrob	7.70e-01								
43	107	6.1	284	2	B39816	myosin heavy chain, f	7.70e-01								
44	107	6.1	676	2	S00084	myosin heavy chain, f	7.70e-01								
45	108	6.1	1947	1	S05697	myosin heavy chain C	5.98e-01								

ALIGNMENTS

RESULT 1

ENTRY I49272 #type complete  
TITLE CD40 receptor-associated factor 1 - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 28-Feb-1997

ACCESSIONS I49272  
REFERENCE A55960  
#authors Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.

#journal Science (1995) 267:1494-1498  
#title Involvement of CRAF1, a relative of TRAF, in CD40 signaling.  
#cross-references M01D:95184010  
#accession I49272

##status preliminary  
##molecule\_type mRNA  
##residues 1-567 ##label RES  
##cross-references EMBL:U21050; NID:g719292; PID:g719293

GENETICS  
#gene CRAF1  
KEYWORDS zinc finger  
SUMMARY #length 567 #molecular-weight 64263 #checksum 4919

Query Match 100.0%; Score 1764; DB 2; Length 567;  
Best Local Similarity 100.0%; Pred. No. 3.34e-278;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 324 SOAEKLKELDKIRPFQNWEEADSMKSSVSLQNRVTELESVDKSAQAARNTGLLESQ 383  
|||  
QY 324 SOAEKLKELDKIRPFQNWEEADSMKSSVSLQNRVTELESVDKSAQAARNTGLLESQ 383  
|||

Db 384 LSRHDTLSVHDIRLADMDLRFQVLETASYNGVLTKIRYKRRKQEAVMGKTLISLXSP 443  
|||  
QY 384 LSRHDTLSVHDIRLADMDLRFQVLETASYNGVLTKIRYKRRKQEAVMGKTLISLXSP 443  
|||

Db 444 FYTGYFGYKMCARYLVNDGMDGKGTSLFVIMRGEVDALLPWFQKQVTKMLMDQSS 503  
|||  
QY 444 FYTGYFGYKMCARYLVNDGMDGKGTSLFVIMRGEVDALLPWFQKQVTKMLMDQSS 503  
|||

Db 504 RHLGDAFKPDNPSSSKPKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKIVDTSD 563  
|||  
QY 504 RHLGDAFKPDNPSSSKPKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKIVDTSD 563  
|||

Db 564 LPD 566  
|||  
QY 564 LPD 566  
|||

```

RESULT 2
ENTRY CD40 receptor-associated factor 1 - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change
DATE 15-Mar-1996

ACCESSIONS A55960
REFERENCE Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
#journal Science (1995) 267:1494-1498
#title Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
#cross-references MUID:95184010
#accession A55960
#status preliminary
#molecule_type mRNA
#residues 1-568 #label RES
#cross-references EMBL:U21092; NID:g726087; PID:g726088

GENETICS
#gene CRAF1
KEYWORDS zinc finger
SUMMARY #length 568 #molecular-weight 64459 #checksum 8765

Query Match 99.4%; Score 1754; DB 2; Length 568;
Best Local Similarity 99.2%; Pred. No. 1.93e-276;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SOAEKLEKELDKETIRPFQNWEEADSKSSVESLQNRVTELESVDKSAGQVARNITGLLESQ 384
QY 324 SOAEKLEKELDKETIRPFQNWEEADSKSSVESLQNRVTELESVDKSAGQVARNITGLLESQ 383
Db 385 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISLQSP 444
QY 384 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISLQSP 443
Db 445 FYTGFGYKMCARVYLNQDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTMLMDQSS 504
QY 444 FYTGFGYKMCARVYLNQDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTMLMDQSS 503
Db 505 RRHGLDAFKDPDPNSSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 564
QY 504 RRHGLDAFKDPDPNSSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 563
Db 565 LPD 567
QY 564 LPD 566

RESULT 3
ENTRY TNFR-associated protein LAP1 - human
TITLE CD40-binding protein
ALTERNATE_NAMES #formal_name Homo sapiens #common_name man
ORGANISM 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
DATE 10-Sep-1997

ACCESSIONS A55649
REFERENCE Mosialos, G.; Birkenbach, M.; Yalamanchilli, R.; VanArsdale, T.; Ware, C.; Kieff, E.
#journal Cell (1995) 80:389-399
#title The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.

#accession A55649
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-568 #label MOS
#cross-references GB:U19260; NID:9675459; PID:g675460
REFERENCE A55135
#authors Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
#journal J. Biol. Chem. (1994) 269:30069-30072
#title A novel RING finger protein interacts with the cytoplasmic

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```

#accession A55135
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-133,135-404,'G',406-568 #label HUA
#cross-references GB:U15637; NID:g595910; PID:g595911
KEYWORDS coiled coil
FEATURE 53-91
SUMMARY #region RING finger motif
#length 568 #molecular-weight 64490 #checksum 8660

Query Match 99.4%; Score 1754; DB 2; Length 568;
Best Local Similarity 99.2%; Pred. No. 1.93e-276;
Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SOAEKLEKELDKETIRPFQNWEEADSKSSVESLQNRVTELESVDKSAGQVARNITGLLESQ 384
QY 324 SOAEKLEKELDKETIRPFQNWEEADSKSSVESLQNRVTELESVDKSAGQVARNITGLLESQ 383
Db 385 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISLQSP 444
QY 384 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISLQSP 443
Db 445 FYTGFGYKMCARVYLNQDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTMLMDQSS 504
QY 444 FYTGFGYKMCARVYLNQDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTMLMDQSS 503
Db 505 RRHGLDAFKDPDPNSSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 564
QY 504 RRHGLDAFKDPDPNSSPKPTGEMNTASGCPVFAQTIVLENGYIYKDDTIFIKVIIVDTSD 563
Db 565 LPD 567
QY 564 LPD 566

RESULT 4
ENTRY CD40-associated protein - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 28-Feb-1997

ACCESSIONS I53498
REFERENCE Sato, T.; Irie, S.; Reed, J.C.
#authors FEBS Lett. (1995) 358:113-118
#journal A novel member of the TRAF family of putative signal
#title transducing proteins binds to the cytosolic domain of CD40.
#cross-references MUID:95129692
#accession I53498
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-543 #label RES
#cross-references GB:U38509; NID:g695357; PID:g695358
GENETICS
#gene CAP-1
SUMMARY #length 543 #molecular-weight 61719 #checksum 5192

Query Match 99.0%; Score 1747; DB 2; Length 543;
Best Local Similarity 98.8%; Pred. No. 3.29e-275;
Matches 240; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 300 SOAEKLEKELDKETIRPFQNWEEADSKSSVESLQNRVTELESVDKSAGQVARNITGLLESQ 359
QY 324 SOAEKLEKELDKETIRPFQNWEEADSKSSVESLQNRVTELESVDKSAGQVARNITGLLESQ 383
Db 360 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISLQSP 419
QY 384 LSRHDOMLSVHDIRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEAVMGKTLISLQSP 443
Db 420 FYTGFGYKMCARVYLNQDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTMLMDQSS 479
QY 444 FYTGFGYKMCARVYLNQDGMKGTHLSLFFVIMRGEYDALLPWPFPKQKVTMLMDQSS 503

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KEYWORDS      homology
FEATURE       hydrolase; metalloproteinase; transmembrane protein; zinc
1-33          #domain signal sequence #status experimental #label SIG\
34-77         #domain propeptide #status experimental #label PRO\
78-760        #product meprin A alpha chain #status experimental
              #label MAT\
87-273        #domain astacin homology #label AST\
276-445       #domain MAM homology #label MAM\
167,171,177,226 #binding_site zinc (His, His, Tyr) #status
              predicted\
168           #active_site Glu #status predicted
SUMMARY       #length 760 #molecular-weight 85702 #checksum 4733

Query Match      9.3%; Score 164; DB 2; Length 760;
Best Local Similarity 30.0%; Pred. No. 7.39e-08;
Matches 27; Conservative 25; Mismatches 34; Indels 4; Gaps 4;

Db 447 VWTIRNISQILENTVKGDKL-V-SPRYNSE-GYGVGVTLYPNGRITNSGLGLAFHLY 503
:| | | : : : | | | : : | | : : | | : : | | : : | | :
QY 418 IWKIRDYKRRKQEAVMGKTLISYQPPYTGFGYKMCARVYLGDMGKTHLSLFFVIM 477
:| | | : : : | | | : : | | : : | | : : | | : : | | :
Db 504 SGNDALPEWPNRQAIMTILDQADTRN 533
:| | | : : : | | | : : | | : : | | : : | | : : | | :
QY 478 RGEYDALLPWPFPKQKVTLM-LMDGSSRRH 506
:| | | : : : | | | : : | | : : | | : : | | : : | | :

RESULT 11
ENTRY   S24134      #type complete
TITLE   endopeptidase 2 (EC 3.4.24.-) - rat
ALTERNATE_NAMES endopeptidase 24.18
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE     02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change
          20-Mar-1998
ACCESSIONS S24134
REFERENCE  S24134
#authors   Corbell, D.; Gaudoux, F.; Wainwright, S.; Ingram, J.; Kenny,
#journal   A.J.; Boileau, G.; Crine, P.
#title     FEBS Lett. (1992) 309:203-208
#cross-references MIM:92371675
#status    preliminary
#molecule_type mRNA
#residues  1-748 #label COR
CLASSIFICATION #superfamily meprin A; astacin homology; EGF homology; MAM
              homology
KEYWORDS      hydrolase; metalloproteinase; zinc
FEATURE       #domain astacin homology #label AST\
76-262        #domain MAM homology #label MAM\
265-434       #binding_site zinc (His) #status predicted\
155,160,166   #active_site Glu #status predicted
157           #length 748 #molecular-weight 85138 #checksum 2333
SUMMARY

Query Match      8.6%; Score 151; DB 2; Length 748;
Best Local Similarity 28.9%; Pred. No. 3.80e-06;
Matches 26; Conservative 23; Mismatches 37; Indels 4; Gaps 4;

Db 436 VWTIRNISQILENTVKGDKL-V-SPRYNSE-GYGVGVTLYPNGRITNSGLGLAFHLY 492
:| | | : : : | | | : : | | : : | | : : | | : : | | :
QY 418 IWKIRDYKRRKQEAVMGKTLISYQPPYTGFGYKMCARVYLGDMGKTHLSLFFVIM 477
:| | | : : : | | | : : | | : : | | : : | | : : | | :
Db 493 SGNDVILEWPNRQAIMTILDQADTRN 522
:| | | : : : | | | : : | | : : | | : : | | : : | | :
QY 478 RGEYDALLPWPFPKQKVTLM-LMDGSSRRH 506
:| | | : : : | | | : : | | : : | | : : | | : : | | :

RESULT 12
ENTRY   HYHUMA      #type complete

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TITLE         meprin A (EC 3.4.24.18) alpha chain precursor - human
ALTERNATE_NAMES intestinal brush border metalloendopeptidase;
                  N-benzoyl-L-tyrosyl-p-aminobenzoic acid hydrolase; PABA
                  peptide hydrolase (PPH) alpha chain
ORGANISM      #formal_name Homo sapiens #common_name man
DATE          19-May-1994 #sequence_revision 16-Feb-1996 #text_change
              05-Sep-1997
ACCESSIONS    S60193; S39464; S39465; A41196
REFERENCE     S60193
#authors      Eldering, J.A.; Grunberg, J.; Sterchi, E.E.
#submission   submitted to the EMBL Data Library, August 1994
#accession    S60193
#molecule_type mRNA
#residues     1-746 #label ELD
#cross-references EMBL:M82962; NID:G535474; PID:G535475
REFERENCE     S39464
#authors      Dumermuth, E.; Eldering, J.A.; Gruenberg, J.; Jiang, W.;
                  Sterchi, E.E.
#journal      FEBS Lett. (1993) 335:367-375
#title        Cloning of the PABA peptide hydrolase alpha subunit
              (PPH-alpha) from human small intestine and its expression
              in COS-1 cells.
#accession    S39464
#molecule_type mRNA
#residues     33-746 #label DUM
#accession    S39465
#molecule_type protein
#residues     66-83 #label DU2
#note         human meprin A alpha chain appears to be expressed in
              intestine but not in kidney
REFERENCE     A41196
#authors      Dumermuth, E.; Sterchi, E.E.; Jiang, W.; Wolz, R.L.; Bond,
                  J.S.; Flannery, A.V.; Beynon, R.J.
#journal      J. Biol. Chem. (1991) 266:21381-21385
#title        The astacin family of metalloendopeptidases.
#cross-references MIM:92042028
#accession    A41196
#molecule_type mRNA
#residues     65-263 #label DU3
#cross-references GB:M82962; GB:M74238
GENETICS      GDB:MEP1A
#gene         #cross-references GDB:371059; OMIM:600388
#map_position 6p21.2-6p21.1
#complex      may form homodimers, homotetramers, or heterotetramers with
              two alpha chains and two beta chains (see HYHUMB)
FUNCTION       zinc metalloproteinase
#description   #superfamily meprin A; astacin homology; EGF homology; MAM
              homology
CLASSIFICATION #glycoprotein; hydrolase; metalloproteinase; transmembrane
              protein; zinc
KEYWORDS
FEATURE       #domain signal sequence #status predicted #label SIG\
1-21          #domain propeptide #status predicted #label PRO\
22-65         #product meprin A alpha chain #status predicted #label
              MAT\
66-746        #domain astacin homology #label AST\
              #domain MAM homology #label MAM\
              #domain EGF homology #label EGF\
              #domain transmembrane #status predicted #label TRM\
75-261        #disulfide_bonds #status predicted\
264-433       #binding_site carbohydrate (Asn) (covalent) #status
              predicted\
674-709       #binding_site zinc (His, His, Tyr) #status
              predicted\
718-740       #active_site Glu #status predicted
107-259,128-147,
674-685,679-694,
696-709       #length 746 #molecular-weight 84367 #checksum 7669
140,222,414,440,
447,539
155,159,165,214
156
SUMMARY       #length 746 #molecular-weight 84367 #checksum 7669
              7.7%; Score 135; DB 1; Length 746;
Query Match

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Query Match          7.5%; Score 132; DB 1; Length 700;
Best Local Similarity 33.3%; Pred. No. 9.47e-04;
Matches 30; Conservative 20; Mismatches 29; Indels 11; Gaps 7;

431 IWHTRNTQFI-GSPNG-TI--YSPPPYSSK-GYAF--QIYLN---LAHVTNAGIYFHLI 480
|||::: : ||| |||::: |||::: |||::: |||::: |||::: |||::: |||:::
418 IWKIRDYKRRKQEAVMGKTLISLQSPYTFYGYKMCARVYLNGDGKMGKTHLSLFFVIM 477
|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
481 SGANDDOLQWPCPQQATWTLLDQNDPIRQ 510
|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
478 RGEYDALLPWPFK-QKVTMLMDQGSRRH 506
|||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::

RESULT 14
ENTRY      #type complete
ENTRY      tropomyosin - migratory locust
TITLE      #formal name Locusta migratoria #common name migratory locust
ORGANISM   03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change
DATE       18-Jun-1993
ACCESSIONS A60364
REFERENCE   A60364
AUTHORS     Krieger, J.; Raming, K.; Knipper, M.; Grau, M.; Mertens, S.;
            Breer, H.
JOURNAL     Insect Biochem. (1990) 20:173-184
TITLE      Cloning, sequencing and expression of locust tropomyosin.
ACCESSION  A60364
STATUS      not compared with conceptual translation
            #molecule_type mRNA
            #residues 1-283 #label KRI
CLASSIFICATION #superfamily tropomyosin
            coiled coil; heptad repeat
KEYWORDS     #length 283 #molecular_weight 32439 #checksum 4917
SUMMARY

Query Match          7.3%; Score 128; DB 2; Length 283;
Best Local Similarity 21.3%; Pred. No. 2.90e-03;
Matches 16; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

41 EPARALQKQIETIENDLQTESLGOVNAKLEEKALQNAESEVALNRRRIQLLEEDLE 100
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
327 EKLKELDKRIRPFRRONWEEA-DSMKSSVESIQNRVTELESVDKSGAQARNTGLLESQLS 385
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
101 RSEERLATATAKLAIE 115
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
386 RHDQTLSDVDFELAD 400
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

RESULT 15
ENTRY      #type complete
ENTRY      meprin A (EC 3.4.24.18) beta chain - rat
TITLE      endopeptidase-2 beta chain; meprin beta chain; meprin-a beta
ALTERNATE_NAMES chain
ORGANISM    #formal_name Rattus norvegicus #common name Norway rat
DATE        17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
            20-Mar-1998
ACCESSIONS  A42908
REFERENCE   A42908
AUTHORS      Johnson, G.D.; Hersh, L.B.
JOURNAL     J. Biol. Chem. (1992) 267:13505-13512
TITLE      Cloning a rat meprin cDNA reveals the enzyme is a
            heterodimer.
            #cross-references MUID:92317075
ACCESSION  A42908
STATUS      preliminary
            #molecule_type mRNA
            #residues 1-668 #label JOH
            sequence extracted from NCBI backbone (NCBIP:107784)
            #note #superfamily meprin A; astacin homology; EGF homology; MAM
            homology
CLASSIFICATION
            heterodimer; hydrolase; metalloproteinase; zinc
KEYWORDS
FEATURE     #domain astacin homology #label AST\
            #domain MAM homology #label MAM\
72-258
261-430

```

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153.157,163,212      #binding_site zinc (His, His, Tyr) #status
                      predicted\
154      #active_site Glu #status predicted
SUMMARY      #length 668 #molecular-weight 75049 #checksum 9806

Query Match      6.9%   Score 121; DB 2; Length 668;
Best Local Similarity 31.6%; Pred.No.1.98e-02;
Matches 24; Conservative 19; Mismatches 26; Indels 7; Gaps 5;

Db      441  LLGGQTVVSPPPYSK-GYAF--QINL--D-LTSPNGLYFHLISGANDQLQWPCPW 494
QY      432  VMGKTLISLYSQPYTVGYGYKMCARYLNGDGMGKGTHTLSLFFVIMRGYDALLPWPFK 490

Db      495  QQATMTLLDQNPDIQ 510
QY      491  QKVTLMMDQSSRRH 506

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